

(TM)

Result No.	Query			ID	Description	Pred. No.	
	Score	Match	Length				
1	107	15.7	325	10	Q39705	1-AMINOCYCLOPROPANE-1-	2.18e-04
2	100	14.6	168	2	Q31938	YONX PROTEIN.	3.43e-03
3	100	14.6	168	9	Q64083	HYPOTHETICAL 19.6 KD P	3.43e-03
4	96	14.1	271	10	Q39960	1-AMINOCYCLOPROPANE-1-	1.58e-02
5	93	13.6	666	2	P72529	PENICILLIN-BINDING PRO	4.86e-02
6	92	13.5	318	10	Q52021	1-AMINOCYCLOPROPANE-1-	7.03e-02
7	91	13.3	282	10	Q64945	ACC OXIDASE 1.	1.02e-01
8	91	13.3	314	10	Q82127	ACC OXIDASE.	1.02e-01
9	91	13.3	417	4	Q399906	DIIC (RHD) (FRAGMENT)	1.02e-01
10	90	13.2	666	2	P72528	PENICILLIN-BINDING PRO	1.46e-01
11	90	13.2	667	4	Q43313	PENICILLIN-BINDING PRO	1.46e-01
12	89	13.0	317	10	Q41681	KTA04031.	2.10e-01
13	89	13.0	481	2	P76052	1-AMINOCYCLOPROPANE-1-	2.10e-01
14	88	12.9	202	1	Q51967	FROM BASES 1389923 TO	3.01e-01
15	88	12.9	666	2	Q54474	ORF H0211.	3.01e-01
16	88	12.7	666	2	Q33681	PENICILIN-BINDING PROT	3.01e-01
17	87	12.7	666	2	P95804	PBP2X (FRAGMENT).	3.01e-01
18	86	12.6	544	1	Q39EG2	PENICILIN-BINDING PROT	4.30e-01
19	85	12.4	318	10	Q43613	544AA LONG HYPOTHETICA	6.13e-01
20	85	12.4	407	6	Q97958	1-AMINOCYCLOPROPANE-1-	8.71e-01
21	85	12.4	318	10	Q97958	RH30-LIKE PROTEIN FRA	8.71e-01

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QY 91 IANI 94

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RESULT 2
ID Q31938 PRELIMINARY; PRT; 168 AA.
AC Q31938;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-AUG-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE YONX PROTEIN.
GN YONX.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE; 98044033.
RA KUNST F., OGASAWARA N., MOSER I., ALBERTINI A.M., ALLONI G.,
RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
RA BORRIS R., BOURSIS L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,
RA BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
RA DENIZOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMERSON P.T.,
RA ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOULGER D.,
RA FRITZ C., FUJITA M., FUJITA Y., FUNA S., GALIZZI A., GALLERON N.,
RA GHIM S.Y., GLASER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G.,
RA GUISEPPI G., GUY B.J., HAGA K., HATECH J., HARWOOD C.R., HENAUT L.,
RA HILBERT H., HOLSAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L.,
RA JORIS B., KARAMATA D., KASAHARA Y., KLAERR-BLANCHARD M., KLEIN C.,
RA KOBATASHI Y., KOETER P., KONINGSSTEIN G., KROGH S., KUMANO M.,
RA KURITA K., LAPIDUS A., LARDINOIS S., LAUBER J., LAZAREVIC V.,
RA LEE S.M., LEVINE A., LIU H., MASUDA S., MAUEL C., MEDIGUE C.,
RA MEDINA N., MELLADO R.P., MIZUNO M., MOESTL D., NAKAI S., NOBACK M.,
RA NOONE D., O'REILLY M., OGAWA K., OGAWA A., OUDEGA B., PARK S.H.,
RA PARRO V., POHL T.M., PORTETELLE D., PORWOLLIK S., PRESCOTT A.M.,
RA PRESCAN E., PUJIC P., PURNELLE B., RAPOPORT G., REY M., REYNOLDS S.,
RA RIEGER M., RIVOLTA C., ROCHA E., ROCHE B., ROSE M., SADAIE Y.,
RA SATO T., SCANLAN E., SCHLEICH S., SCHROETER R., SCOFFONE F.,
RA SEKIGUCHI J., SEKOWSKA A., SEROT S.J., SERROR P., SHIN B.S., SOLDADO B.,
RA SOROKIN A., TACCONI E., TAKAGI T., TAKAHASHI H., TAKEMARU K.,
RA TOSATO V., UCHIYAMA S., VANDENBOL M., VANNIER F., VASSAROTTI A.,
RA VIARI A., WAMBUIT R., WEDLER E., WEDLER H., WEITZENEGGER T.,
RA WINTERS P., WIPAT A., YAMAMOTO H., YAMANE K., YASUMOTO K., YATA K.,
RA YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A.,
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis".
RL Nature 390:249-256(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; J99113; CAB4013.1; -.
SQ SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;
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Query Match 14.6%; Score 100; DB 2; Length 168;
Best Local Similarity 24.1%; Pred. No. 3.43e-03;
Matches 21; Conservative 29; Mismatches 32; Indels 5; Gaps 5;

Db 15 LENEINTQYCELDTNLDALSKNRILESOLEKFESSLTNRLOGSISNNCRNDLLNLGYTH 74
: : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | |
QY 13 IOGSVLTSTCE-RTN-GGYNTSSIDLNSVNIENVDSGL-KWQPSNFETCRNTOLA-GSSE 68
: : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | |
Db 75 SQVDCMSDEEVAALD-KIDEETHNTD 100
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 69 LAAECKTRAQQFVSTKINLDDHIANID 95
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RESULT 3  
ID Q64083 PRELIMINARY; PRT; 168 AA.

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AC Q64083;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE HYPOTHETICAL 19.6 KD PROTEIN.
GN YONX.
OS Bacteriophage SPBc2.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.
RN [1]
RP SEQUENCE FROM N.A.
RA LAZAREVIC V., DUSTERHOFT A., SOLDADO B., HILBERT H., MAUEL C.,
RA KARAMATA D.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF020713; AAC13043.1; -.
KW Hypothetical protein.
SQ SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;
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Query Match 14.6%; Score 100; DB 9; Length 168;
Best Local Similarity 24.1%; Pred. No. 3.43e-03;
Matches 21; Conservative 29; Mismatches 32; Indels 5; Gaps 5;

Db 15 LENEINTQYCELDTNLDALSKNRILESOLEKFESSLTNRLOGSISNNCRNDLLNLGYTH 74
: : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | |
QY 13 IOGSVLTSTCE-RTN-GGYNTSSIDLNSVNIENVDSGL-KWQPSNFETCRNTOLA-GSSE 68
: : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | |
Db 75 SQVDCMSDEEVAALD-KIDEETHNTD 100
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 69 LAAECKTRAQQFVSTKINLDDHIANID 95
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RESULT 4
ID Q39960 PRELIMINARY; PRT; 271 AA.
AC Q39960;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE 1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID OXIDASE (FRAGMENT).
GN ACO OR ACCO2.
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Asteridae; euasterids II; Asterales; Asteraceae;
OC Asteroideae; Heliantheae; Helianthus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97435977.
RA LIU J.H., LEE-TAMON S.H., REID D.M.;
RT "Differential and wound-inducible expression of 1-aminocyclopropane-1-
RT carboxylate oxidase genes in sunflower seedlings.";
RL Plant Mol. Biol. 34:923-933(1997).
DR EMBL; U62554; AAC49824.1; -.
DR MENDEL; 8463; Helan; ACO:8463.
DR PFAM; PF00671; Fe_Asc-oxidored; 1.
FT NON_TER 1
FT NON_TER 271
SQ SEQUENCE 271 AA; 31079 MW; 01B8149C CRC32;
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Query Match 14.1%; Score 96; DB 10; Length 271;
Best Local Similarity 20.6%; Pred. No. 1.58e-02;
Matches 13; Conservative 22; Mismatches 27; Indels 1; Gaps 1;

Db 41 ASKGLAVQNVQIDD-LDWESTFYIRHLPESNISEIPDLEDEYKVMREFAKELEKLAENI 99
: : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | |
QY 32 SSIDLNSVNIENVDSGLKWQPSNFETCRNTQLAGSSELAAECKTRAQQFVSTKINLDDHI 91
: : | | | : : : | | | : : : | | | : : : | | | : : : | | | : : : | | |
Db 100 LDI 102
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 92 ANI 94
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RESULT 5  
ID P72529 PRELIMINARY; PRT; 666 AA.  
AC P72529;

[illegible]

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE; 96269518.
RA BECKERS E.A., FRAS B.H., LIGHART P., SIMSEK S., OVERBEEK M.A.,
RA DEM BORNE A.E., VAN RHENEN D.J., DER SCHOOT C.E.;
RT "Characterization of the hybrid RHD gene leading to the partial D
RT category IIc phenotype.";
RL Transfusion 36:567-574(1996).
RN [2]
RP SEQUENCE OF 1-49 FROM N.A.
RA MEDLINE; 96420256.
RA HUANG C.H.;
RT "Alteration of RH gene structure and expression in human dCce and
RT DCW-red blood cells: phenotypic homozygosity versus genotypic
RT heterozygosity.";
RL Blood 88:2326-2333(1996).
DR EMBL; S82449; AAB37696.1; -.
DR EMBL; S83379; CAB34097.1; -.
DR PFAM; PF00909; Ammonium_transp; 1.
FT NON_TER 417
SQ SEQUENCE 417 AA; 45099 MW; BCB0B58F CRC32;

Query Match 13.3%; Score 91; DB 4; Length 417;
Best Local Similarity 22.6%; Pred. No. 1.02e-01;
Matches 21; Conservative 31; Mismatches 36; Indels 5; Gaps 5;

Db 221 PSFNALLRPIERKNVNTYYAV-VSVTAISGSSLAHPQKISKTYVHSVAVLAGGV 279
QY 11 SAIOGSVLTCTERTNGYNTS-SIDLNSVINDVGS-LKWQPSNFIETC-RNTQLAGSS 67

Db 280 AVGTSCHLIPSPWLAWLGLVAGLSVGA-KY 311
QY 68 ELAAECKTRAQOFVSTKINLDDHIANIDGTLKY 100

RESULT 10
ID P72528 PRELIMINARY; PRT; 666 AA.
AC P72528
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE PENICILLIN-BINDING PROTEIN (FRAGMENT).
GN PBP2X.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HUI1;
RA REICHMAN P., KOENIG A., MARTON A., HAKENBECK R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X98365; CAAG7011.1; -.
DR PFAM; PF00905; Transpeptidase; 1.
FT NON_TER 1
FT NON_TER 666
SQ SEQUENCE 666 AA; 72761 MW; 0BFBAD9A CRC32;

Query Match 13.2%; Score 90; DB 2; Length 666;
Best Local Similarity 29.8%; Pred. No. 1.46e-01;
Matches 28; Conservative 23; Mismatches 37; Indels 6; Gaps 5;

Db 88 DASVEGIDFTTPNRSYPNGQFASFLAQLAHENEDGS-KSLGTFGLESSLNTILAGT 146
QY 10 NSAIQGSVLTCTERT--NGGYNTSSIDLNSVINDVGS-LKWQPSNFIETC-RNTQLAGS 66

Db 147 DGIITYEKDRVGNIVPGT-ELVSQ-QTVDGKDVY 178
QY 67 SELAAECKTRAQOFVSTKINLDDHIANIDGTLKY 100

RESULT 11

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ID O43313 PRELIMINARY; PRT; 667 AA.
AC O43313
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE KIAA0431.
DE KIAA0431.
GN KIAA0431.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA ISHIIKAWA K., NAGASE T., NAKAJIMA D., SEKI N., OHIRA M., MIYAJIMA N.,
RA TANAKA A., KOTANI H., NOMURA N., OHARA O.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB007891; BAA24861.1; -.
DR PFAM; PF00096; zf-C2H2; 2.
DR PFAM; PF00096; zf-C2H2; 2.
SQ SEQUENCE 667 AA; 72334 MW; 19900DE9 CRC32;

Query Match 13.2%; Score 90; DB 4; Length 667;
Best Local Similarity 22.9%; Pred. No. 1.46e-01;
Matches 16; Conservative 21; Mismatches 31; Indels 2; Gaps 2;

Db 243 LGNTCQRNSSISINVQDLSYASQNFPSAQWATADSVSSCSTDLSPDSQVSLPISVH 302
QY 18 LTSTCETNGGYNTSSIDLNSVINDVGS-LKWQPSNFIETC-RNTQLAGSSLAEECKTR 76

Db 303 TOTELPSSKV 312
QY 77 AQFV-STKI 85

RESULT 12
ID O41681 PRELIMINARY; PRT; 317 AA.
AC O41681
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG.
GN ACO.
OS Phascolus aureus (Mung bean) (Vigna radiata).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
OC Vigna.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-HYPOCOTYL;
RX MEDLINE; 94339795.
RA KIM W.T., YANG S.F.;
RT "Structure and expression of cDNAs encoding 1-aminocyclopropane-1-
RT carboxylate oxidase homologs isolated from excised mung bean
RT hypocotyls.";
RL Planta 194:223-229(1994).
DR EMBL; U06046; AAC48921.1; -.
DR MENDEL; 504; Phaa; ACO; 504.
DR PFAM; PF00671; Fe_Asc_Oxidore; 1.
SQ SEQUENCE 317 AA; 35773 MW; F02B6272 CRC32;

Query Match 13.0%; Score 89; DB 10; Length 317;
Best Local Similarity 18.6%; Pred. No. 2.10e-01;
Matches 11; Conservative 21; Mismatches 26; Indels 1; Gaps 1;

Db 74 LESVQSEIND-LWSESTFFLRHLPSVNSVNTDLDDQYRKIMKQFAEELEKLAHLDDL 131
QY 36 LNSVINDVGS-LKWQPSNFIETC-RNTQLAGSSLAEECKTRAQOFVSTKINLDDHIANI 94

RESULT 13
ID P76052 PRELIMINARY; PRT; 481 AA.
AC P76052
DT 01-FEB-1997 (Tremblrel. 02, Created)

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DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)  
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)  
 DE FROM BASES 1389923 TO 1402712  
 DE (SECTION 121 OF 400) OF THE COMPLETE GENOME (SECTION 121 OF 400).  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K-12;  
 RX MEDLINE; 97426617.  
 RA BLATTNER F.R., PLUNKETT III G., BLOCH C.A., PERNA N.T., BURLAND V.,  
 RA RILEY M., COLLADO-VIDES J., GLASNER J.D., RODE C.K., MAYHEW G.F.,  
 RA GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,  
 RA MAU B., SHAO Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 DR EMBL; AE000231; AAC74419.1;  
 SO SEQUENCE 481 AA; 52193 MW; 8C5C0196 CRC32;  
 [5] Sequence Match 13.0%; Score 89; DB 2; Length 481;  
 Best Local Similarity 30.0%; Pred. No. 2.10e-01;  
 Matches 12; Conservative 12; Mismatches 16; Indels 0; Gaps 0;  
 Db 136 GTVRFYCGPGEGGKTFMVREGVDDVDAALTWHPF 175  
 QY 15 GSVLTSCRTNGYNTSSIDLSNVGSLKQWQSNF 54  
 RESULT 14  
 ID OS1967 PRELIMINARY; PRT; 202 AA.  
 AC OS1967;  
 DT 01-JUN-1998 (Tremblrel. 06, Created)  
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)  
 DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)  
 DE ORF H0211.  
 OS Halobacterium sp.  
 OC Plasmid pNRC100.  
 OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;  
 OC Halobacterium.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NRC-1;  
 RX MEDLINE; 88201675.  
 RA DASSARMA S., DAMERVAL T., JONES J.G., TANDEAU DE MARSAC N.;  
 RT "A plasmid-encoded gas vesicle protein gene in a halophilic  
 archaeobacterium.";  
 RL Mol. Microbiol. 1:365-370(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NRC-1;  
 RX MEDLINE; 90016863.  
 RA JONES J.G., HACKETT N.R., HALLADAY J.T., SCOTHORN D.J., YANG C.F.,  
 RA NG W.L., DASSARMA S.;  
 RT "Analysis of insertion mutants reveals two new genes in the pNRC100  
 gas vesicle gene cluster of Halobacterium halobium.";  
 RL Nucleic Acids Res. 17:7783-7793(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NRC-1;  
 RX MEDLINE; 91267967.  
 RA NG W.L., KOTHAKOTA S., DASSARMA S.;  
 RT "Structure of the gas vesicle plasmid in Halobacterium halobium  
 inversion isomers, inverted repeats, and insertion sequences.";  
 RL J. Bacteriol. 173:3933-3933(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NRC-1;  
 RX MEDLINE; 91323716.  
 RA JONES J.G., YOUNG D.C., DASSARMA S.;  
 RT "Structure and organization of the gas vesicle gene cluster on the  
 Halobacterium halobium plasmid pNRC100.";  
 RL Gene 102:117-122(1991).

RN [5] SEQUENCE FROM N.A.  
 RP STRAIN-NRC-1;  
 RX MEDLINE; 93012964.  
 RA HALLADAY J.T., NG W.L., DASSARMA S.;  
 RT "Genetic transformation of a halophilic archaeobacterium with a gas  
 vesicle gene cluster restores its ability to float.";  
 RL Gene 119:131-136(1992).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NRC-1;  
 RX MEDLINE; 93139036.  
 RA HALLADAY J.T., JONES J.G., LIN F., MACDONALD A.B., DASSARMA S.;  
 RT "The rightward gas vesicle operon in Halobacterium plasmid pNRC100:  
 identification of the gvpA and gvpC gene products by use of antibody  
 probes and genetic analysis of the region downstream of gvpC.";  
 RL J. Bacteriol. 175:684-692(1993).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NRC-1;  
 RX MEDLINE; 93327890.  
 RA DASSARMA S.;  
 RT "Identification and analysis of the gas vesicle gene cluster on an  
 unstable plasmid of Halobacterium halobium.";  
 RL Experientia 49:482-486(1993).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NRC-1;  
 RX MEDLINE; 93328662.  
 RA NG W.L., DASSARMA S.;  
 RT "Minimal replication origin of the 200-kilobase Halobacterium plasmid  
 pNRC100.";  
 RL J. Bacteriol. 175:4584-4596(1993).  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NRC-1;  
 RX MEDLINE; 95095934.  
 RA DASSARMA S., ARORA P., LIN F., MOLINARI E., YIN L.R.;  
 RT "Wild-type gas vesicle formation requires at least ten genes in the  
 gvp gene cluster of Halobacterium halobium plasmid pNRC100.";  
 RL J. Bacteriol. 176:7646-7652(1994).  
 RN [10]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NRC-1;  
 RX MEDLINE; 95095934.  
 RA DASSARMA S., ARORA P., DASSARMA S.;  
 RL Syst. Appl. Microbiol. 16:560-568(1994).  
 RN [11]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NRC-1;  
 RX MEDLINE; 95095934.  
 RA DASSARMA S.;  
 RL (in) Robb F.T., Place A.R., Sowers K.R., Schreier H.J., Dassarma S.,  
 RL Fleischmann E.M. (eds.);  
 RL Archaea:  
 RL A laboratory manual - halophiles, pp.253-255,  
 RL Cold Spring Harbor Laboratory Press, New York (1995).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NRC-1;  
 RX MEDLINE; 95095934.  
 RA DASSARMA S., ARORA P.;  
 RL FEWS Microbiol. Lett. 153:1-10(1997).  
 RN [13]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NRC-1;  
 RX MEDLINE; 95095934.  
 RA NG W.L., CIUFFO S.A., SMITH T.M., BUMGARDNER R.E., LORETZ C., BASKIN D.,  
 RA FAUST J., SETO J., SLAGEL J., HOOD L., DASSARMA S.;  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 RN [14]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NRC-1;  
 RX MEDLINE; 95095934.  
 RA NG W.L., CIUFFO S.A., SMITH T.M., BUMGARDNER R.E., LORETZ C., BASKIN D.,  
 RA FAUST J., SETO J., SLAGEL J., HOOD L., DASSARMA S.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF016485; AAC82797.1;

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